



SEQUENCE LISTING

CHEN, HONG-HWA
 TSAI, WEN-CHIEH

<120> GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID

<130> U 014863-8

<140> 10/690,246

<141> 2003-10-21

<150> 091125320

<151> 2002-10-25

<160> 24

<170> PatentIn version 3.2

<210> 1

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<212> DNA

<213> Phalaenopsis equestris

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aat ccg acg aac agg caa gtt aca tat tct aag agg aga gtt ggg ata      159
Asn Pro Thr Asn Arg Gln Val Thr Tyr Ser Lys Arg Arg Val Gly Ile
      15              20              25

ctg aag aag gcc aag gag ctc act gtt ctc tgt gat gct cag gtc tct      207
Leu Lys Lys Ala Lys Glu Leu Thr Val Leu Cys Asp Ala Gln Val Ser
      30              35              40

ctc atc atg ttc tca agc aca gga aag ttg gct gat tac tgc agc ccc      255
Leu Ile Met Phe Ser Ser Thr Gly Lys Leu Ala Asp Tyr Cys Ser Pro
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tct act gat att aag ggg ata tat gag agg tac cag gtt gtg act gga      303
Ser Thr Asp Ile Lys Gly Ile Tyr Glu Arg Tyr Gln Val Val Thr Gly
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atg gat cta tgg aat gct cag tat gag agg atg cag aat acg ctg aag      351
Met Asp Leu Trp Asn Ala Gln Tyr Glu Arg Met Gln Asn Thr Leu Lys
      80              85              90

cat ctg aat gag att aac caa aac ctg agg aag gag att agg agg agg      399
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Lys	Gly	Glu	Glu	Leu	Glu	Gly	Met	Asp	Ile	Lys	Gln	Leu	Arg	Gly	Leu		
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Glu	Gln	Thr	Leu	Glu	Glu	Ser	Leu	Arg	Ile	Val	Arg	His	Arg	Lys	Tyr		
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Thr	Arg	Glu	Thr	Tyr	Arg	Ala	Leu	Ile	His	Glu	Leu	Asp	Met	Lys	Glu		
			160					165					170				
gag	aat	ccg	aac	tac	ggg	ttt	aat	gta	gaa	aac	cag	agt	aga	att	tat		639
Glu	Asn	Pro	Asn	Tyr	Gly	Phe	Asn	Val	Glu	Asn	Gln	Ser	Arg	Ile	Tyr		
	175						180					185					
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Glu	Asn	Ser	Ile	Pro	Met	Val	Asn	Glu	Cys	Pro	Gln	Met	Phe	Ser	Phe		
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Arg	Val	Val	His	Pro	Asn	Gln	Pro	Asn	Leu	Leu	Gly	Leu	Gly	Tyr	Glu		
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Ser	His	Asp	Leu	Ser	Leu	Ala											
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Lys Glu Leu Thr Val Leu Cys Asp Ala Gln Val Ser Leu Ile Met Phe
35 40 45

Ser Ser Thr Gly Lys Leu Ala Asp Tyr Cys Ser Pro Ser Thr Asp Ile
50 55 60

Lys Gly Ile Tyr Glu Arg Tyr Gln Val Val Thr Gly Met Asp Leu Trp
65 70 75 80

Asn Ala Gln Tyr Glu Arg Met Gln Asn Thr Leu Lys His Leu Asn Glu
85 90 95

Ile Asn Gln Asn Leu Arg Lys Glu Ile Arg Arg Arg Lys Gly Glu Glu
100 105 110

Leu Glu Gly Met Asp Ile Lys Gln Leu Arg Gly Leu Glu Gln Thr Leu
115 120 125

Glu Glu Ser Leu Arg Ile Val Arg His Arg Lys Tyr His Val Ile Ala
130 135 140

Thr Gln Thr Asp Thr Tyr Lys Lys Lys Leu Lys Ser Thr Arg Glu Thr
145 150 155 160

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165 170 175

Tyr Gly Phe Asn Val Glu Asn Gln Ser Arg Ile Tyr Glu Asn Ser Ile
180 185 190

Pro Met Val Asn Glu Cys Pro Gln Met Phe Ser Phe Arg Val Val His
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gcaagaaaga gaacc atg ggg agg ggg aag atc gag ata aag aag att gag	231
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Ile Asn Leu Trp Ser Glu Gln Tyr Glu Lys Met Gln Asn Thr Leu Asn	
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cac gtc atc agc acc cag aca gat aca ttc aaa aaa aag ttg aaa aac	663
His Val Ile Ser Thr Gln Thr Asp Thr Phe Lys Lys Lys Leu Lys Asn	
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gca ctt gga aat ggg gct tcc tac ttg tat tca ttt cgt acc caa cca	807
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85 90 95	
Ile Asn His Asn Leu Arg Arg Glu Ile Arg Gln Arg Met Gly Glu Asp	
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Leu Glu Gly Leu Glu Ile Lys Glu Leu Arg Gly Leu Glu Gln Asn Met	
115 120 125	

Asp Glu Ala Leu Lys Leu Val Arg Asn Arg Lys Tyr His Val Ile Ser
130 135 140

Thr Gln Thr Asp Thr Phe Lys Lys Lys Leu Lys Asn Ser Gln Glu Thr
145 150 155 160

His Arg Asn Leu Leu Arg Glu Leu Glu Thr Glu His Ala Val Tyr Tyr
165 170 175

Val Asp Asp Asp Pro Asn Asn Tyr Asp Gly Ala Leu Ala Leu Gly Asn
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agctttcttc ctcatctctc ccgttcgtca acatcactaa tcaactgctgt ttcagtagac 180
tgaggagagct aggagtggag aaaagagatt tgaag atg ggg agg ggg aag ata 233
Met Gly Arg Gly Lys Ile
1 5
gag att aag aag ata gag aat ccg act aat cgg cag gtg acc tac tcg 281
Glu Ile Lys Lys Ile Glu Asn Pro Thr Asn Arg Gln Val Thr Tyr Ser
10 15 20
aag agg aga gct ggg att atg aag aag gcg agg gag atc act gtt ctc 329
Lys Arg Arg Ala Gly Ile Met Lys Lys Ala Arg Glu Ile Thr Val Leu
25 30 35
tgc gat gct gag gtt tcg ctt atc atg ttc tcg agt act ggg aag ttt 377
Cys Asp Ala Glu Val Ser Leu Ile Met Phe Ser Ser Thr Gly Lys Phe

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55	60	65	70
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Tyr Gln Gln Val Ser Gly Ile Asn Leu Trp Ser Ser Gln Tyr Glu Lys			
	75	80	85
atg ctg aat acg ctt aac cat tcg aag gag atc aat cgc aat ctg agg			521
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	90	95	100
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Arg Glu Val Arg Gln Arg Met Gly Glu Asp Leu Glu Gly Leu Asp Ile			
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aag gaa ctg cgc ggt ctt gag caa aac att gat gag gca ttg aag cta			617
Lys Glu Leu Arg Gly Leu Glu Gln Asn Ile Asp Glu Ala Leu Lys Leu			
	120	125	130
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Val Arg Asn Arg Lys Tyr His Val Ile Ser Thr Gln Thr Asp Thr Tyr			
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Lys Lys Lys Leu Lys Asn Ser Gln Glu Thr His Arg Asn Leu Met His			
	155	160	165
gaa ttg gaa atc gtt gag gac cac cca gtg tat ggg ttc cac gag gat			761
Glu Leu Glu Ile Val Glu Asp His Pro Val Tyr Gly Phe His Glu Asp			
	170	175	180
tca agc aat tat gag ggt gtt ctt gct ctt gca aat gac ggg tct cac			809
Ser Ser Asn Tyr Glu Gly Val Leu Ala Leu Ala Asn Asp Gly Ser His			
	185	190	195
atg tat gcc ttc cgg gtg caa ccc aac caa caa aat ctt caa gga acg			857
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Gly Tyr Ser Ser His Asp Leu Arg Leu Ala			
	215	220	
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Lys Lys Val Phe Glu Arg Tyr Gln Gln Val Ser Gly Ile Asn Leu Trp
65 70 75 80

Ser Ser Gln Tyr Glu Lys Met Leu Asn Thr Leu Asn His Ser Lys Glu
85 90 95

Ile Asn Arg Asn Leu Arg Arg Glu Val Arg Gln Arg Met Gly Glu Asp
100 105 110

Leu Glu Gly Leu Asp Ile Lys Glu Leu Arg Gly Leu Glu Gln Asn Ile
115 120 125

Asp Glu Ala Leu Lys Leu Val Arg Asn Arg Lys Tyr His Val Ile Ser
130 135 140

Thr Gln Thr Asp Thr Tyr Lys Lys Lys Leu Lys Asn Ser Gln Glu Thr
145 150 155 160

His Arg Asn Leu Met His Glu Leu Glu Ile Val Glu Asp His Pro Val
165 170 175

Tyr Gly Phe His Glu Asp Ser Ser Asn Tyr Glu Gly Val Leu Ala Leu
180 185 190

Ala Asn Asp Gly Ser His Met Tyr Ala Phe Arg Val Gln Pro Asn Gln
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Gln Asn Leu Gln Gly Thr Gly Tyr Ser Ser His Asp Leu Arg Leu Ala
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 Met Gly Arg Gly Lys Ile Glu Ile Lys Lys Ile Glu Asn Pro Thr
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 agc agg caa gta acg tat tca aag agg cga ctt ggg atc atg aag aag 215
 Ser Arg Gln Val Thr Tyr Ser Lys Arg Arg Leu Gly Ile Met Lys Lys
 20 25 30
 gca gag gaa ctc aca gtg ctc tgc gac gct caa ctc tca ctc atc atc 263
 Ala Glu Glu Leu Thr Val Leu Cys Asp Ala Gln Leu Ser Leu Ile Ile
 35 40 45
 ttc tca agc tcc ggc aag tta gct gat ttc tgc agc cct tcc aca gac 311
 Phe Ser Ser Ser Gly Lys Leu Ala Asp Phe Cys Ser Pro Ser Thr Asp
 50 55 60
 gtt aaa gat ata gtt gag agg tac caa aat gtt acc gga att gat ata 359
 Val Lys Asp Ile Val Glu Arg Tyr Gln Asn Val Thr Gly Ile Asp Ile
 65 70 75
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 Trp Asp Ala Gln Tyr Gln Arg Met Gln Asn Thr Leu Arg Asn Leu Arg
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 Glu Ile Asn Arg Asn Leu Gln Lys Glu Ile Arg Gln Arg Lys Gly Glu
 100 105 110
 aat ctg gaa ggg ttg ggc gtt aaa gag ctg cgc ggt ctt gag caa aaa 503
 Asn Leu Glu Gly Leu Gly Val Lys Glu Leu Arg Gly Leu Glu Gln Lys
 115 120 125
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 Leu Glu Glu Ser Val Lys Ile Val Arg Gln Arg Lys Tyr His Val Ile
 130 135 140
 gct acg caa aca gac act tgc agg aaa aag ctc aaa agc agc aga caa 599
 Ala Thr Gln Thr Asp Thr Cys Arg Lys Lys Leu Lys Ser Ser Arg Gln
 145 150 155

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160					165					170					175	

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Ser	Ile	Ser	Met	Ala	Asn	Arg	Leu	His	Arg	Ser	Glu	Pro	Asn	Val	Gln	
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35 40 45

Lys Asp Ile Val Glu Arg Tyr Gln Asn Val Thr Gly Ile Asp Ile Trp
65 70 75 80

Ile Asn Arg Asn Leu Gln Lys Glu Ile Arg Gln Arg Lys Gly Glu Asn
100 105 110

115

120

125

Glu Glu Ser Val Lys Ile Val Arg Gln Arg Lys Tyr His Val Ile Ala
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Thr Gln Thr Asp Thr Cys Arg Lys Lys Leu Lys Ser Ser Arg Gln Ile
 145 150 155 160

Tyr Arg Ala Leu Thr His Glu Leu Gln Lys Leu Asp Glu Glu Asn Gln
 165 170 175

Pro Cys Ser Phe Leu Val Glu Asp Leu Ser Cys Ile Tyr Asp Ser Ser
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